

SEQUENCE LISTING

<110> Braun, Ralph P.
Thomsen, Lindy
Van-Wely, Catherine
Ertl, Peter

<120> Adjuvant

<130> 033267-015

<140> US 10/102,622

<141> 2002-03-19

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> HBsAg in BALB/C mice

<400> 1

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu
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<210> 2

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> HSV CD8 in BALB/C mice

<400> 2

His Gly Pro Ser Leu Tyr Arg Thr Phe
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<210> 3

<211> 1503

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of the p55 gag insert in
pGagOptpr2

<400> 3

atgggtgccc gagcttcggt actgtctggt ggagagctgg acagatggga gaaaattagg 60
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cttgaacggt ttgccgtgaa cccaggcctg ctggaaacat ctgagggatg tcgccagatc 180
ctggggcaat tgcagccatc cctccagacc gggagtgaag agctgaggtc cttgtataac 240

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acagtggcta ccctctactg cgtacaccag aggatcgaga ttaaggatac caaggaggcc 300
ttggacaaaa ttgaggagga gcaaaacaag agcaagaaga aggccagca ggcagctgct 360
gacactgggc atagcaacca ggtatcacag aactatccta ttgtccaaaa cattcagggc 420
cagatggttc atcaggccat cagcccccg acgctcaatg cctgggtgaa ggttgctgaa 480
gagaaggcct tttctcctga ggttatcccc atgttctccg ctttgagtga gggggccact 540
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tacaagggga gactcgttaa tttcctgcaa agcaggcccc agcccaccgc ccccctgag 1380
gaatccttca ggtccggagt ggagaccaca acgcctcccc aaaaacagga accaatcgac 1440
aaggagctgt accctttaac ttctctgcgt tctctctttg gcaacgaccc gtcgtctcaa 1500
taa 1503

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<210> 4

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of p55 gag insert in
pGagOptpr2

<400> 4

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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
 20          25          30
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
 35          40          45
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
 50          55          60
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
 65          70          75          80
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
 85          90          95
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100          105          110
Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
115          120          125
Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
130          135          140
Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145          150          155          160
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
165          170          175
Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
180          185          190
Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
195          200          205

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Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
 210 215 220
 Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
 225 230 235 240
 Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
 245 250 255
 Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
 260 265 270
 Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
 275 280 285
 Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 290 295 300
 Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
 305 310 315 320
 Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
 325 330 335
 Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
 340 345 350
 Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
 355 360 365
 Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
 370 375 380
 Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
 385 390 395 400
 Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
 405 410 415
 Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
 420 425 430
 Phe Leu Gly Lys Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe
 435 440 445
 Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg
 450 455 460
 Ser Gly Val Glu Thr Thr Thr Pro Pro Gln Lys Gln Glu Pro Ile Asp
 465 470 475 480
 Lys Glu Leu Tyr Pro Leu Thr Ser Leu Arg Ser Leu Phe Gly Asn Asp
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 Pro Ser Ser Gln
 500

<210> 5

<211> 1515

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of the p17/24trNEF insert in
p17/24trNEF1

<400> 5

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 ctagaacgat tcgcagttaa tcctggcctg ttagaacat cagaaggctg tagacaaata 180
 ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240
 acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct 300
 ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct 360
 gacacaggac acagcaatca ggtcagccaa aattacccta tagtcagaa catccagggg 420
 caaatggtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa 480
 gagaaggctt tcagcccaga agtgataccc atgttttcag cattatcaga aggagccacc 540

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ccacaagatt taaacacccat gctaaacaca gtgggggggac atcaagcagc catgcaaattg 600
ttaaaaagaga ccatcaatga ggaagctgca gaatgggata gagtgcattcc agtgcattgca 660
gggcctattg caccaggcca gatgagagaa ccaaggggaa gtgacatagc aggaactact 720
agtacccttc aggaacaaat aggatggatg acaaataatc cacctatccc agtaggagaa 780
atttataaaa gatggataat cctgggatta aataaaatag taagaatgta tagccctacc 840
agcattctgg acataagaca aggaccaaaa gaacccttta gagactatgt agaccggttc 900
tataaaactc taagagccga gcaagcttca caggaggtaa aaaattggat gacagaaacc 960
ttgttgggtcc aaaatgcgaa cccagattgt aagactatct taaagcattt gggaccagcg 1020
gctacactag aagaaatgat gacagcatgt cagggagtag gaggaccggg ccataaggca 1080
agagtttttg tgggttttcc agtcacacct caggtacctt taagaccaat gacttacaag 1140
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tcccaaagaa gacaagatat ccttgatctg tggatctacc acacacaagg ctacttcctt 1260
gattggcaga actacacacc agggccaggg gtcagatata cactgacctt tggatggtgc 1320
tacaagctag taccagttga gccagataag gtagaagagg ccaataaagg agagaacacc 1380
agcttggttac accctgtgag cctgcatggg atggatgacc cggagagaga agtgtttagag 1440
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ttcaagaact gctga 1515

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<210> 6

<211> 504

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of the p17/24trNEF insert in
p17/24trNEF1

<400> 6

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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20     25     30
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35     40     45
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50     55     60
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65     70     75     80
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85     90     95
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Gln Asn Lys Ser Lys
100    105    110
Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
115    120    125
Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
130    135    140
Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145    150    155    160
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
165    170    175
Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
180    185    190
Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
195    200    205
Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
210    215    220
Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225    230    235    240
Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile

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		275					280					285			
Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu
	290					295					300				
Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr
305					310					315				320	
Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala
			325						330					335	
Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly
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Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Val	Gly	Phe	Pro	Val
	355						360					365			
Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met	Thr	Tyr	Lys	Ala	Ala	Val	Asp
370						375					380				
Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly	Leu	Glu	Gly	Leu	Ile	His
385					390					395				400	
Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp	Leu	Trp	Ile	Tyr	His	Thr	Gln
			405					410						415	
Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	Pro	Gly	Pro	Gly	Val	Arg
		420						425					430		
Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys	Leu	Val	Pro	Val	Glu	Pro
	435						440					445			
Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly	Glu	Asn	Thr	Ser	Leu	Leu	His
	450					455					460				
Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro	Glu	Arg	Glu	Val	Leu	Glu
465					470					475				480	
Trp	Arg	Phe	Asp	Ser	His	Leu	Ala	Phe	His	His	Val	Ala	Arg	Glu	Leu
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			500												

<210> 7

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of the p17/24opt/trNef insert
in p17/24opt/trNef1

<400> 7

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cttgaacggt	ttgccgtgaa	cccaggcctg	ctggaaacat	ctgagggatg	tcgccagatc	180
ctggggcaat	tgcagccatc	cctccagacc	gggagtgaag	agctgaggtc	cttgtataac	240
acagtggcta	ccctctactg	cgtacaccag	aggatcgaga	ttaaggatac	caaggaggcc	300
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cagatggttc	atcaggccat	cagcccccg	acgctcaatg	cctgggtgaa	ggttgtcgaa	480
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tctacactgc	aagagcaa	cggatggatg	accaacaatc	ctcccatccc	agttggagaa	780
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<210> 8

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of the p17/24opt/trNef insert
in p17/24opt/trNef1

<400> 8

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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
      20          25          30
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
      35          40          45
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
      50          55          60
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
      65          70          75          80
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
      85          90          95
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Gln Asn Lys Ser Lys
      100          105          110
Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
      115          120          125
Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
      130          135          140
Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
      145          150          155          160
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
      165          170          175
Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
      180          185          190
Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
      195          200          205
Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
      210          215          220
Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
      225          230          235          240
Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
      245          250          255
Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
      260          265          270
Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
      275          280          285

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Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
290                               295           300
Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305                               310           315           320
Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
325                               330           335
Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
340                               345           350
Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Met Val Gly Phe Pro
355                               360           365
Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val
370                               375           380
Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile
385                               390           395           400
His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr
405                               410           415
Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val
420                               425           430
Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu
435                               440           445
Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu
450                               455           460
His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu Val Leu
465                               470           475           480
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485                               490           495
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500                               505

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<210> 9

<211> 1689

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of RT insert of p7077-RT3

<400> 9

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accgagatgg agaaagaggg caagatcagc aagatcgggc ctgagaaccc atacaacacc 180
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aagaagcatc agaaggagcc gccattcctg tggatgggct acgagctcca tcccgacaag 720
tggaaccgtg agcctatcgt cctccccgag aaggacagct ggaccgtgaa cgacatccag 780
aagctggtgg gcaagctcaa ctgggctagc cagatctatc ccgggatcaa ggtgcgccag 840
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ggcgcccaca ccaacgatgt caagcagctg accgaggccg tccagaagat caccaccgag 1140
tccatcgtga tctgggggaa gacacccaag ttcaagctgc ctatccagaa ggagacctgg 1200

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agccagtacg cgctgggcat tattcaggcc cagccggacc agtccgagag cgaactggtg 1560
aaccagatta tcgagcagct gatcaagaaa gagaaggctt acctgcctg ggtcccggcc 1620
cataagggca ttggcgga caagcaggtc gacaagctgg tgagtgcggg gattagaaa 1680
gtgctgtaa 1689

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<210> 10

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of RT insert of p7077-RT3

<400> 10

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Met Gly Pro Ile Ser Pro Ile Glu Thr Val Ser Val Lys Leu Lys Pro
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Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys
20     25     30
Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys
35     40     45
Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala
50     55     60
Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg
65     70     75     80
Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
85     90     95
Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp
100    105    110
Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys
115    120    125
Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile
130    135    140
Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala
145    150    155    160
Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln
165    170    175
Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly
180    185    190
Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg
195    200    205
Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln
210    215    220
Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys
225    230    235    240
Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val
245    250    255
Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
260    265    270
Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr
275    280    285
Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu
290    295    300
Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
305    310    315    320

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Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
 325 330 335
 Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
 340 345 350
 Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
 355 360 365
 Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile
 370 375 380
 Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp
 385 390 395 400
 Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp
 405 410 415
 Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu
 420 425 430
 Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala
 435 440 445
 Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly
 450 455 460
 Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu
 465 470 475 480
 Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn
 485 490 495
 Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro
 500 505 510
 Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile
 515 520 525
 Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile
 530 535 540
 Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys
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 Val Leu

<210> 11

<211> 1689

<212> DNA

<213> Artificial Sequence

<220>

 <223> nucleotide sequence of the coding insert in
 p73i-RT3

<400> 11

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accgagatgg agaaagaggg caagatcagc aagatcgggc ctgagaaccc atacaacacc 180
cccgtgtttg ccatcaagaa gaaggacagc accaagtggc gcaagctggt ggatttcgg 240
gagctgaata agcggaccca ggatttctgg gaggtccagc tgggcatccc ccatccggcc 300
ggcctgaaga agaagaagag cgtgaccgtg ctggacgtgg gcgacgctta cttcagcgtc 360
cctctggacg aggacttttag aaagtacacc gcctttacca tcccatttat caacaacgag 420
accctggca tcagatatca gtacaacgtc ctccccagc gctggaaggg ctctcccgcc 480
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cgcacgaaga ttgaggagct gaggcagcat ctgctgagat ggggcctgac cactccggac 660
aagaagcatc agaaggagcc gccattcctg tggatgggct acgagctcca tcccagacaag 720
tgaccgtgc agcctatcgt cctccccgag aaggacagct ggaccgtgaa cgacatccag 780
aagctggtgg gcaagctcaa ctgggctagc cagatctatc ccgggatcaa ggtgcgccag 840
ctctgcaagc tgctgcgcgg caccaaggcc ctgaccgagg tgattcccct cacggaggaa 900

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gccgagctcg agctggctga gaaccgggag atcctgaagg agcccgtgca cggcgtgtac 960
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ggcgcccaca ccaacgatgt caagcagctg accgaggccg tccagagatg cagcaccgag 1140
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gagacgtggt ggaccgaata ttggcaggcc acctggattc ccgagtggga gttcgtgaat 1260
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agccagtacg cgctgggcat tattcaggcc cagccggacc agtccgagag cgaactggag 1560
aaccagatta tcgagcagct gatcaagaaa gagaaggctt acctcgctg ggtcccggcc 1620
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<210> 12

<211> 561

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of the coding insert in
p73i-RT3

<400> 12

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Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile
 35          40          45
Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile
 50          55          60
Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu
 65          70          75          80
Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro
 85          90          95
His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val
100          105          110
Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr
115          120          125
Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg
130          135          140
Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile
145          150          155          160
Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn
165          170          175
Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser
180          185          190
Asp Leu Glu Ile Gly Gln His Thr Arg Lys Ile Glu Glu Leu Arg Gln
195          200          205
His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys
210          215          220
Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp
225          230          235          240
Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val Asn
245          250          255
Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr
260          265          270

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Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys
 275 280 285
 Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu
 290 295 300
 Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr
 305 310 315 320
 Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly
 325 330 335
 Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr
 340 345 350
 Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln
 355 360 365
 Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp
 370 375 380
 Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu
 385 390 395 400
 Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu
 405 410 415
 Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys
 420 425 430
 Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn
 435 440 445
 Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly Arg
 450 455 460
 Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu Leu
 465 470 475 480
 Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn Ile
 485 490 495
 Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro Asp
 500 505 510
 Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile Lys
 515 520 525
 Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile Gly
 530 535 540
 Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys Val
 545 550 555 560
 Leu

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